**Contents of ChIP-Seq**

**Shell script files** (ending in .sh)

Chip\_compare.sh

Spombe\_macs.sh

Spombe\_broad.sh

fastQC.sh

trim\_adaptors.sh

TruSeq2-PE.fa – this is a file of the most common adapters used for trimming

**Raw\_data\_11.16.2020**

* These are the files downloaded from the sequencing facility (in the novogene directory)
* Each sample has two files associated with it in its own directory

**Trimmed\_fq\_11.16.2020**

* These files are fastq files trimmed of adapters

**Trimmed\_fastq\_reports**

* These have html and zip files, the html files can be opened in any browser to review fastqc statistics on the trimmed fastq files

**Bwa\_bamfiles**

* These are alignment files (bam) and their appropriate index files (bai) from trimmed fastq files using the software bwa
* Allsummary.txt shows the alignment statistics for each sample

**Bw\_files**

* The log2 comparison files able to be viewed on a genome browser
* Cluster1bedfiles
  + These are bed files (can also be visualized on genome browser) that refer to genes with the strongest narrow peaks after hierarchical clustering was performed

**Macs2\_output**

* These are the xls output of narrow peaks for each sample compared to the input using the software MACS2
* **Peak\_genes\_bedfiles**
  + These are the bed files for each of the peaks found from Macs2

**Macs2\_broad output**

* These are the xls output of broad beaks for each sample compared to the input using the software MACS2
* **Peak\_genes\_bedfiles**
* These are the bed files for each of the broad peaks found from Macs2